



SEQUENCE LISTING

<110> Skeiky, Yasir
Reed, Steven
Alderson, Mark
Corixa Corporation

<120> Fusion Proteins of Mycobacterium Tuberculosis

<130> 014058-009050US

<140> US 09/597,796

<141> 2000-06-20

<150> US 09/056,556

<151> 1998-04-07

<150> US 09/223,040

<151> 1998-12-30

<150> WO PCT/US99/07717

<151> 1999-04-07

<150> US 09/287,849

<151> 1999-04-07

<150> US 60/158,338

<151> 1999-10-07

<150> US 60/158,425

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<160> 30

<170> PatentIn Ver. 2.1

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<212> DNA

<213> Mycobacterium tuberculosis

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<223> Ra35, N-terminus of MTB32A (TbRa35FL)

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<221> CDS

<222> (1) .. (588)

<223> Ra35

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 <212> PRT
 <213> Mycobacterium tuberculosis

<220>
 <223> Ra35, N-terminus of MTB32A (TbRa35FL)

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 35 40 45
 Gly Ile Val Ile Asp Pro Asn Gly Val Val Leu Thr Asn Asn His Val
 50 55 60
 Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe Ser Val Gly Ser Gly Gln
 65 70 75 80
 Thr Tyr Gly Val Asp Val Val Gly Tyr Asp Arg Thr Gln Asp Val Ala
 85 90 95
 Val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala Ile Gly
 100 105 110
 Gly Gly Val Ala Val Gly Glu Pro Val Val Ala Met Gly Asn Ser Gly
 115 120 125
 Gly Gln Gly Gly Thr Pro Arg Ala Val Pro Gly Arg Val Val Ala Leu
 130 135 140
 Gly Gln Thr Val Gln Ala Ser Asp Ser Leu Thr Gly Ala Glu Glu Thr
 145 150 155 160
 Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala Ile Gln Pro Gly Asp Ser
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 Ala Ala Ser
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 <213> Mycobacterium tuberculosis

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 <223> MTB32A (TbRa35FL) cDNA

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 <222> (1460)
 <223> n = g, a, c or t

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 <222> (1854)
 <223> n = g, a, c or t

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 gtcacgtgtg ctgagcgtgc tggctgccgt cgggctgggc ctggccacgg cgccggccca 180
 ggcggccccc cggccttgt cgcaggaccg gtgcgccgac ttccccgcgc tgcccctcga 240
 cccgtccgcg atggtcgccc aagtggcgcc acagggtggtc aacatcaaca ccaaactggg 300

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 <212> PRT
 <213> Mycobacterium tuberculosis

<220>
 <223> MTB32A (TbRa35FL) protein

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Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe Ala Asp Phe Pro Ala Leu
 35          40          45
Pro Leu Asp Pro Ser Ala Met Val Ala Gln Val Ala Pro Gln Val Val
 50          55          60
Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn Ala Val Gly Ala Gly Thr
 65          70          75          80
Gly Ile Val Ile Asp Pro Asn Gly Val Val Leu Thr Asn Asn His Val
 85          90          95
Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe Ser Val Gly Ser Gly Gln
100          105          110
Thr Tyr Gly Val Asp Val Val Gly Tyr Asp Arg Thr Gln Asp Val Ala
115          120          125
Val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala Ile Gly
130          135          140
Gly Gly Val Ala Val Gly Glu Pro Val Val Ala Met Gly Asn Ser Gly
145          150          155          160
Gly Gln Gly Gly Thr Pro Arg Ala Val Pro Gly Arg Val Val Ala Leu
165          170          175

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Gly Gln Thr Val Gln Ala Ser Asp Ser Leu Thr Gly Ala Glu Glu Thr
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 195 200 205
 Gly Gly Pro Val Val Asn Gly Leu Gly Gln Val Val Gly Met Asn Thr
 210 215 220
 Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe Ala
 225 230 235 240
 Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser Gly
 245 250 255
 Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly Leu
 260 265 270
 Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val Val
 275 280 285
 Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val Ile
 290 295 300
 Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala Asp
 305 310 315 320
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 <212> DNA
 <213> Mycobacterium tuberculosis

<220>
 <223> MTBRa12 C-terminus of MTB32A (Ra35FL)

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 caccgttcat atcgggccta ccgccttctt cggttgggt gttgtcgaca acaacggcaa 180
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 cgcgcttaac gggcatcatc ccggtgacgt catctcggtg aactggcaaa ccaagtcggg 360
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 ataccaccgc ccggccggcc aattgga 447

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 <212> PRT
 <213> Mycobacterium tuberculosis

<220>
 <223> MTBRa12 C-terminus of MTB32A (Ra35FL)

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 20 25 30
 Gly Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly
 35 40 45

Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val
 50 55 60
 Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val
 65 70 75 80
 Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala
 85 90 95
 Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Asn Trp
 100 105 110
 Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu
 115 120 125
 Gly Pro Pro Ala
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<210> 7
 <211> 3058
 <212> DNA
 <213> Mycobacterium tuberculosis

<220>
 <223> MTB39 (TbH9) cDNA full-length

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<211> 391
<212> PRT
<213> Mycobacterium tuberculosis

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<220>
<223> MTB39 (TbH9) protein full-length

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Asp Ser Val Ala Ser Asp Leu Phe Ser Ala Ala Ser Ala Phe Gln Ser
      35          40          45
Val Val Trp Gly Leu Thr Val Gly Ser Trp Ile Gly Ser Ser Ala Gly
      50          55          60
Leu Met Val Ala Ala Ala Ser Pro Tyr Val Ala Trp Met Ser Val Thr
      65          70          75          80
Ala Gly Gln Ala Glu Leu Thr Ala Ala Gln Val Arg Val Ala Ala Ala
      85          90          95
Ala Tyr Glu Thr Ala Tyr Gly Leu Thr Val Pro Pro Pro Val Ile Ala
      100          105          110
Glu Asn Arg Ala Glu Leu Met Ile Leu Ile Ala Thr Asn Leu Leu Gly
      115          120          125
Gln Asn Thr Pro Ala Ile Ala Val Asn Glu Ala Glu Tyr Gly Glu Met
      130          135          140
Trp Ala Gln Asp Ala Ala Ala Met Phe Gly Tyr Ala Ala Ala Thr Ala
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Thr Ala Thr Ala Thr Leu Leu Pro Phe Glu Glu Ala Pro Glu Met Thr
      165          170          175
Ser Ala Gly Gly Leu Leu Glu Gln Ala Ala Val Glu Glu Ala Ser
      180          185          190
Asp Thr Ala Ala Ala Asn Gln Leu Met Asn Asn Val Pro Gln Ala Leu
      195          200          205
Gln Gln Leu Ala Gln Pro Thr Gln Gly Thr Thr Pro Ser Ser Lys Leu
      210          215          220
Gly Gly Leu Trp Lys Thr Val Ser Pro His Arg Ser Pro Ile Ser Asn
      225          230          235          240
Met Val Ser Met Ala Asn Asn His Met Ser Met Thr Asn Ser Gly Val
      245          250          255
Ser Met Thr Asn Thr Leu Ser Ser Met Leu Lys Gly Phe Ala Pro Ala
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305					310					315					320
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				325					330					335	
Ala	Leu	Pro	Leu	Thr	Ser	Leu	Thr	Ser	Ala	Ala	Glu	Arg	Gly	Pro	Gly
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 <223> MTB59F

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 <212> PRT
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<220>
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 protein TbH9-Ra35 (MTB59F)

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 20 25 30
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 35 40 45
 Ser Ala Ala Ser Ala Phe Gln Ser Val Val Trp Gly Leu Thr Val Gly
 50 55 60
 Ser Trp Ile Gly Ser Ser Ala Gly Leu Met Val Ala Ala Ala Ser Pro
 65 70 75 80
 Tyr Val Ala Trp Met Ser Val Thr Ala Gly Gln Ala Glu Leu Thr Ala
 85 90 95
 Ala Gln Val Arg Val Ala Ala Ala Ala Tyr Glu Thr Ala Tyr Gly Leu
 100 105 110
 Thr Val Pro Pro Pro Val Ile Ala Glu Asn Arg Ala Glu Leu Met Ile
 115 120 125
 Leu Ile Ala Thr Asn Leu Leu Gly Gln Asn Thr Pro Ala Ile Ala Val
 130 135 140
 Asn Glu Ala Glu Tyr Gly Glu Met Trp Ala Gln Asp Ala Ala Ala Met
 145 150 155 160
 Phe Gly Tyr Ala Ala Thr Ala Thr Ala Thr Ala Thr Leu Leu Pro
 165 170 175
 Phe Glu Glu Ala Pro Glu Met Thr Ser Ala Gly Gly Leu Leu Glu Gln
 180 185 190
 Ala Ala Ala Val Glu Glu Ala Ser Asp Thr Ala Ala Ala Asn Gln Leu
 195 200 205
 Met Asn Asn Val Pro Gln Ala Leu Gln Gln Leu Ala Gln Pro Thr Gln
 210 215 220
 Gly Thr Thr Pro Ser Ser Lys Leu Gly Gly Leu Trp Lys Thr Val Ser
 225 230 235 240
 Pro His Arg Ser Pro Ile Ser Asn Met Val Ser Met Ala Asn Asn His
 245 250 255
 Met Ser Met Thr Asn Ser Gly Val Ser Met Thr Asn Thr Leu Ser Ser
 260 265 270
 Met Leu Lys Gly Phe Ala Pro Ala Ala Ala Gln Ala Val Gln Thr
 275 280 285
 Ala Ala Gln Asn Gly Val Arg Ala Met Ser Ser Leu Gly Ser Ser Leu
 290 295 300
 Gly Ser Ser Gly Leu Gly Gly Gly Val Ala Ala Asn Leu Gly Arg Ala
 305 310 315 320
 Ala Ser Val Gly Ser Leu Ser Val Pro Gln Ala Trp Ala Ala Ala Asn
 325 330 335
 Gln Ala Val Thr Pro Ala Ala Arg Ala Leu Pro Leu Thr Ser Leu Thr
 340 345 350
 Ser Ala Ala Glu Arg Gly Pro Gly Gln Met Leu Gly Gly Leu Pro Val
 355 360 365
 Gly Gln Met Gly Ala Arg Ala Gly Gly Gly Leu Ser Gly Val Leu Arg
 370 375 380
 Val Pro Pro Arg Pro Tyr Val Met Pro His Ser Pro Ala Ala Gly Asp
 385 390 395 400


```

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gagtcacaac cgtgggtcggg agcgctccgg cggcaagtct cggcatctcc accggcgcac 300
tgatcaccgc ggtcgacggc gtcctgatca actcggccac cgcgatggcg gacgcgtta 360
acgggcatca tcccgggtgac gtcctctcgg tgacctggca aaccaagtcg ggcggcacgc 420
gtacagggaa cgtgacattg gccgagggac ccccgggcga attcatggtg gatttcgggg 480
cgttaccacc ggagatcaac tccgcgagga tgtacgcccg cccgggttcg gcctcgttg 540
tggccgcggc tcagatgtgg gacagcgtgg cgagtgcctt gttttcggcc gcgtcggcgt 600
ttcagtcggt ggtctggggg ctgacgggtg ggtcgtggat aggttcgtcg gcgggtctga 660
tggtggcggc ggcctcgccg tatgtggcgt ggatgagcgt caccgcgggg caggccgagc 720
tgaccgcggc ccagggtccg gttgctgcgg cggcctacga gacggcgtat gggctgacgg 780
tgcccccgcc ggtgatcgcc gagaaccgtg ctgaactgat gattctgata gcgaccaacc 840
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cgttcagcgt cggctccggc caaacctacg gcgtcgatgt ggtcgggtat gaccgcaccc 1920
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cgctgaccgg tgccgaagag acattgaacg ggttgatcca gttcgatgcc gcgatccagc 2160
ccggtgattc gggcgggccc gtcgtcaacg gcctaggaca ggtggtcgg atgaacacgg 2220
ccgcgtccta ggatatccat cacactggcg gccgctcgag cagatccggn tgtaacaaag 2280
cccgaaa
2287

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<210> 12
<211> 729
<212> PRT
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence:fusion
protein Ra12-TbH9-Ra35 (MTB72F)

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<400> 12
Met His His His His His Thr Ala Ala Ser Asp Asn Phe Gln Leu
  1             5             10             15
Ser Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala
             20             25             30
Ile Ala Gly Gln Ile Arg Ser Gly Gly Gly Ser Pro Thr Val His Ile
             35             40             45
Gly Pro Thr Ala Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn
             50             55             60
Gly Ala Arg Val Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu
             65             70             75             80
Gly Ile Ser Thr Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile
             85             90             95

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Asn	Ser	Ala	Thr	Ala	Met	Ala	Asp	Ala	Leu	Asn	Gly	His	His	Pro	Gly
			100					105					110		
Asp	Val	Ile	Ser	Val	Thr	Trp	Gln	Thr	Lys	Ser	Gly	Gly	Thr	Arg	Thr
		115					120					125			
Gly	Asn	Val	Thr	Leu	Ala	Glu	Gly	Pro	Pro	Ala	Glu	Phe	Met	Val	Asp
	130					135					140				
Phe	Gly	Ala	Leu	Pro	Pro	Glu	Ile	Asn	Ser	Ala	Arg	Met	Tyr	Ala	Gly
145					150					155					160
Pro	Gly	Ser	Ala	Ser	Leu	Val	Ala	Ala	Ala	Gln	Met	Trp	Asp	Ser	Val
				165					170					175	
Ala	Ser	Asp	Leu	Phe	Ser	Ala	Ala	Ser	Ala	Phe	Gln	Ser	Val	Val	Trp
			180					185					190		
Gly	Leu	Thr	Val	Gly	Ser	Trp	Ile	Gly	Ser	Ser	Ala	Gly	Leu	Met	Val
		195					200					205			
Ala	Ala	Ala	Ser	Pro	Tyr	Val	Ala	Trp	Met	Ser	Val	Thr	Ala	Gly	Gln
	210					215					220				
Ala	Glu	Leu	Thr	Ala	Ala	Gln	Val	Arg	Val	Ala	Ala	Ala	Ala	Tyr	Glu
225					230					235					240
Thr	Ala	Tyr	Gly	Leu	Thr	Val	Pro	Pro	Pro	Val	Ile	Ala	Glu	Asn	Arg
				245				250						255	
Ala	Glu	Leu	Met	Ile	Leu	Ile	Ala	Thr	Asn	Leu	Leu	Gly	Gln	Asn	Thr
			260					265					270		
Pro	Ala	Ile	Ala	Val	Asn	Glu	Ala	Glu	Tyr	Gly	Glu	Met	Trp	Ala	Gln
		275				280						285			
Asp	Ala	Ala	Ala	Met	Phe	Gly	Tyr	Ala	Ala	Ala	Thr	Ala	Thr	Ala	Thr
	290					295					300				
Ala	Thr	Leu	Leu	Pro	Phe	Glu	Glu	Ala	Pro	Glu	Met	Thr	Ser	Ala	Gly
305					310					315					320
Gly	Leu	Leu	Glu	Gln	Ala	Ala	Ala	Val	Glu	Glu	Ala	Ser	Asp	Thr	Ala
				325					330					335	
Ala	Ala	Asn	Gln	Leu	Met	Asn	Asn	Val	Pro	Gln	Ala	Leu	Gln	Gln	Leu
			340					345					350		
Ala	Gln	Pro	Thr	Gln	Gly	Thr	Thr	Pro	Ser	Ser	Lys	Leu	Gly	Gly	Leu
		355				360						365			
Trp	Lys	Thr	Val	Ser	Pro	His	Arg	Ser	Pro	Ile	Ser	Asn	Met	Val	Ser
	370					375					380				
Met	Ala	Asn	Asn	His	Met	Ser	Met	Thr	Asn	Ser	Gly	Val	Ser	Met	Thr
385					390					395					400
Asn	Thr	Leu	Ser	Ser	Met	Leu	Lys	Gly	Phe	Ala	Pro	Ala	Ala	Ala	Arg
				405					410					415	
Gln	Ala	Val	Gln	Thr	Ala	Ala	Gln	Asn	Gly	Val	Arg	Ala	Met	Ser	Ser
			420				425						430		
Leu	Gly	Ser	Ser	Leu	Gly	Ser	Ser	Gly	Leu	Gly	Gly	Gly	Val	Ala	Ala
		435				440					445				
Asn	Leu	Gly	Arg	Ala	Ala	Ser	Val	Gly	Ser	Leu	Ser	Val	Pro	Gln	Ala
	450					455					460				
Trp	Ala	Ala	Ala	Asn	Gln	Ala	Val	Thr	Pro	Ala	Ala	Arg	Ala	Leu	Pro
465					470					475					480
Leu	Thr	Ser	Leu	Thr	Ser	Ala	Ala	Glu	Arg	Gly	Pro	Gly	Gln	Met	Leu
				485				490						495	
Gly	Gly	Leu	Pro	Val	Gly	Gln	Met	Gly	Ala	Arg	Ala	Gly	Gly	Gly	Leu
			500					505					510		
Ser	Gly	Val	Leu	Arg	Val	Pro	Pro	Arg	Pro	Tyr	Val	Met	Pro	His	Ser
		515					520					525			
Pro	Ala	Ala	Gly	Asp	Ile	Ala	Pro	Pro	Ala	Leu	Ser	Gln	Asp	Arg	Phe
	530					535					540				
Ala	Asp	Phe	Pro	Ala	Leu	Pro	Leu	Asp	Pro	Ser	Ala	Met	Val	Ala	Gln
545					550					555					560
Val	Gly	Pro	Gln	Val	Val	Asn	Ile	Asn	Thr	Lys	Leu	Gly	Tyr	Asn	Asn
				565					570					575	

Ala Val Gly Ala Gly Thr Gly Ile Val Ile Asp Pro Asn Gly Val Val
580 585 590
Leu Thr Asn Asn His Val Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe
595 600 605
Ser Val Gly Ser Gly Gln Thr Tyr Gly Val Asp Val Val Gly Tyr Asp
610 615 620
Arg Thr Gln Asp Val Ala Val Leu Gln Leu Arg Gly Ala Gly Gly Leu
625 630 635 640
Pro Ser Ala Ala Ile Gly Gly Gly Val Ala Val Gly Glu Pro Val Val
645 650 655
Ala Met Gly Asn Ser Gly Gly Gln Gly Thr Pro Arg Ala Val Pro
660 665 670
Gly Arg Val Val Ala Leu Gly Gln Thr Val Gln Ala Ser Asp Ser Leu
675 680 685
Thr Gly Ala Glu Glu Thr Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala
690 695 700
Ile Gln Pro Gly Asp Ser Gly Gly Pro Val Val Asn Gly Leu Gly Gln
705 710 715 720
Val Val Gly Met Asn Thr Ala Ala Ser
725

<210> 13
<211> 500
<212> DNA
<213> Mycobacterium tuberculosis

<220>
<223> Mtb8.4 (DPV)

<400> 13
cgtggcaatg tcgttgaccg tcggggccgg ggtcgccctcc gcagatcccg tggacgcggg 60
cattaacacc acctgcaatt acgggcaggt agtagctgcg ctcaacgcga cggatccggg 120
ggctgccgca cagttcaacg cctcaccggg ggcgcagtcg tatttgcgca atttcctcgc 180
cgcaccgcca cctcagcgcg ctgccatggc cgcgcaattg caagctgtgc cgggggcggc 240
acagtacatc ggccttgctg agtcggttgc cggctcctgc aacaactatt aagcccatgc 300
gggccccatc ccgcgacccg gcatcgctgc cggggctagg ccagattgcc ccgctcctca 360
acgggcccga tcccgcgacc cggcatcgtc gccggggcta ggccagattg ccccgctcct 420
caacggggcc catctcgtgc cgaattcctg cagccccggg gatccactag ttctagagcg 480
gccgccaccg cggtgaggct 500

<210> 14
<211> 96
<212> PRT
<213> Mycobacterium tuberculosis

<220>
<223> Mtb8.4 (DPV)

<400> 14
Val Ala Met Ser Leu Thr Val Gly Ala Gly Val Ala Ser Ala Asp Pro
1 5 10 15
Val Asp Ala Val Ile Asn Thr Thr Cys Asn Tyr Gly Gln Val Val Ala
20 25 30
Ala Leu Asn Ala Thr Asp Pro Gly Ala Ala Ala Gln Phe Asn Ala Ser
35 40 45
Pro Val Ala Gln Ser Tyr Leu Arg Asn Phe Leu Ala Ala Pro Pro Pro
50 55 60
Gln Arg Ala Ala Met Ala Ala Gln Leu Gln Ala Val Pro Gly Ala Ala
65 70 75 80

Gln Tyr Ile Gly Leu Val Glu Ser Val Ala Gly Ser Cys Asn Asn Tyr
85 90 95

<210> 15
<211> 585
<212> DNA
<213> Mycobacterium tuberculosis

<220>
<223> Mtb9.8 (MSL)

<400> 15
tggattccga tagcgggtttc ggccccctcga cgggcgacca cggcgcgag gcctccgaac 60
ggggggccgg gacgctggga ttccgcccga cgcgaaccaa agaacgccgg gtccggggcg 120
tcgggctgac cgcactggcc ggtgatgagt tcggcaacgg cccccggatg ccgatgggtgc 180
cggggacctg ggagcagggc agcaacgagc ccgagggcgc cgacggatcg gggagagggg 240
gaggcgacgg cttaccgcac gacagcaagt aaccgaattc cgaatcacgt ggaccctac 300
gggtcgaaaag gagagatgtt atgagccttt tggatgctca tatccacag ttggtggcct 360
cccagtcggc gtttgccgcc aaggcggggc tgatgcggca cagcatcggc caggccgagc 420
aggcggcgat gtcggctcag gcgtttcacc agggggagtc gtcggcggcg tttcaggccg 480
cccatgcccg gtttggtggc gcggccgcca aagtcaacac cttgttggat gtcgcgcagg 540
cgaatctggg tgaggccgcc ggtacctatg tggccgccga tgctg 585

<210> 16
<211> 97
<212> PRT
<213> Mycobacterium tuberculosis

<220>
<223> Mtb9.8 (MSL)

<400> 16
Met Ser Leu Leu Asp Ala His Ile Pro Gln Leu Val Ala Ser Gln Ser
1 5 10 15
Ala Phe Ala Ala Lys Ala Gly Leu Met Arg His Thr Ile Gly Gln Ala
20 25 30
Glu Gln Ala Ala Met Ser Ala Gln Ala Phe His Gln Gly Glu Ser Ser
35 40 45
Ala Ala Phe Gln Ala Ala His Ala Arg Phe Val Ala Ala Ala Ala Lys
50 55 60
Val Asn Thr Leu Leu Asp Val Ala Gln Ala Asn Leu Gly Glu Ala Ala
65 70 75 80
Gly Thr Tyr Val Ala Asp Ala Ala Ala Ser Thr Tyr Thr Gly
85 90 95
Phe

<210> 17
<211> 1742
<212> DNA
<213> Mycobacterium tuberculosis

<220>
<223> Mtb9.9A (MTI, MTI-A)

<220>
<221> modified_base
<222> (1)..(1742)
<223> n = g, a, c or t

<400> 17
 ccgctctctt tcaacgtcat aagttcgggtg ggccagtcgg ccgcgcgtgc atatggcacc 60
 aataacgcgt gtcccatgga tacccgacc gcacgacggt agagcggatc agcgagccg 120
 gtgccgaaca ctaccgcgtc cacgctcagc cctgccgcgt tgcggaagat cgagcccagg 180
 ttctcatggt cgттаacgcc ttccaacact gcgacggtgc gcgccccggc gaccacctga 240
 gcaacgctcg gctccggcac ccggcgcgcg gctgccaaaca cccacgatt gagatggaag 300
 ccgatcacc gtgccatgac atcagccgac gctcgatagt acggcgcgcc gacaccggcc 360
 agatcatcct tgagctcggc cagccggcgg tcggtgccga acagcgccag cggcgtgaac 420
 cgtgaggcca gcatgcgctg caccaccagc acaccctcgg cgatcaccaa cgccttgccg 480
 gtcggcagat cgggacnacn gtcgatgctg ttcaggtcac ggaaatcgtc gagccgtggg 540
 tcgctcgggat cgcagacgtc ctgaacatcg aggcgcgtcg ggtgctgggc acaacggcct 600
 tcggtcacgg gctttcgtcg accagagcca gcatcagatc ggcggcgctg cgcaggatgt 660
 cacgctcgct gcggttcagc gtcgcgagcc gctcagccag ccactcttgc agagagccgt 720
 tgctgggatt aattgggaga ggaagacagc atgtcgttcg tgaccacaca gccggaagcc 780
 ctggcagctg cggcggcgaa cctacagggg attggcacga caatgaacgc ccagaacgcg 840
 gccgcggctg ctccaaccac cggagtagtg cccgcagccg ccgatgaagt atcagcgctg 900
 accgcggctc agtttgctgc gcacgcgag atgtaccaa cggtcagcgc ccaggccgcg 960
 gccattcacg aaatgttcgt gaacacgctg gtggccagtt ctggctcata cgcggccacc 1020
 gaggcggcca acgcagccgc tgccggctga acgggctcgc acgaacctgc tgaaggagag 1080
 ggggaacatc cggagttctc gggtcagggg ttgcgccagc gccagccga ttcagntatc 1140
 ggcgtccata acagcagacg atctaggcat tcagtactaa ggagacaggc aacatggcct 1200
 cacgttttat gacggatccg catgcgatgc gggacatggc gggccggttt gaggtgcacg 1260
 cccagacggg ggagggacgag gctcgccgga tgtggcgctc cgcgcaaaac atttcgggtg 1320
 cgggctggag tggcatggcc gaggcgacct cgctagacac catgacctag atgaatcagg 1380
 cgtttcgcaa catcgtgaac atgtgcacg ggggtcgtga cgggctggtt cgcgacgcca 1440
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 cacagctgng tacgntttct cacattagga gaacaccaat atgacgatta attaccagtt 1560
 cggggacgct gacgctcatg gcgccatgat ccgcgctcag gcggcgctgc ttgaggcgga 1620
 gcatcaggcc atcgttcgtg atgtgttggc cgcgggtgac ttttggggcg gcgccggttc 1680
 ggtggcttgc caggagtcca ttaccagtt gggccgtaac ttccaggtga tctacgagca 1740
 99 1742

<210> 18
 <211> 94
 <212> PRT
 <213> Mycobacterium tuberculosis

<220>
 <223> Mtb9.9A (MTI, MTI-A)

<400> 18
 Met Thr Ile Asn Tyr Gln Phe Gly Asp Val Asp Ala His Gly Ala Met
 1 5 10 15
 Ile Arg Ala Leu Ala Gly Leu Leu Glu Ala Glu His Gln Ala Ile Ile
 20 25 30
 Ser Asp Val Leu Thr Ala Ser Asp Phe Trp Gly Gly Ala Gly Ser Ala
 35 40 45
 Ala Cys Gln Gly Phe Ile Thr Gln Leu Gly Arg Asn Phe Gln Val Ile
 50 55 60
 Tyr Glu Gln Ala Asn Ala His Gly Gln Lys Val Gln Ala Ala Gly Asn
 65 70 75 80
 Asn Met Ala Gln Thr Asp Ser Ala Val Gly Ser Ser Trp Ala
 85 90

<210> 19
 <211> 1200
 <212> DNA
 <213> Mycobacterium tuberculosis

<220>

<223> MTB40 (HTCC#1) cDNA

<400> 19

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caggcatgag cagagcgttc atcatcgatc caacgatcag tgccattgac ggcttgtacg 60
accttctggg gattggaata cccaaccaag ggggtatcct ttactcctca ctagagtact 120
tcgaaaaagc cctggaggag ctggcagcag cgtttccggg tgatggctgg ttaggttcgg 180
ccgcggacaa atacgccggc aaaaaccgca accacgtgaa ttttttccag gaactggcag 240
acctcgatcg tcagctcatc agcctgatcc acgaccaggc caacgcgggtc cagacgaccc 300
gcgacatcct ggagggcgcc aagaaaggtc tcgagttcgt gcgcccgggtg gctgtggacc 360
tgacctacat cccggtcgtc gggcacgccc tatcggccgc cttccaggcg ccgttttgcg 420
cgggcgcgat ggccgtagtg ggcggcgcgc ttgcctactt ggtcgtgaaa acgctgatca 480
acgcgactca actcctcaaa ttgcttgcca aattggcgga gttggtcgcg gccgccattg 540
cggacatcat ttcggatgtg gcggacatca tcaagggcac cctcggagaa gtgtgggagt 600
tcatcacaaa cgcgctcaac ggcctgaaag agctttggga caagctcacg ggggtgggtga 660
ccggactgtt ctctcgaggg tggtcgaacc tggagtcctt ctttgccggc gtccccggct 720
tgaccggcgc gaccagcggc ttgtcgcaag tgactggctt gttcgggtgcg gccggtctgt 780
ccgcacgctc gggcttggct cagcgggata gcctggcgag ctcagccagc ttgcccgccc 840
tgggccggcat tgggggcggg tccggttttg ggggcttgcc gagcctggct caggtccatg 900
ccgcctcaac tcggcaggcg ctacggcccc gagctgatgg cccggtcggc gccgctgccg 960
agcaggctcg cgggcagtcg cagctggctc ccgcgcaggg ttcccaagg atgggcggac 1020
ccgtaggcat gggcggcgat caccctctt cgggggcgct gaaaggagcg acgacgaaga 1080
agtactcgga aggcgcggcg gcgggactg aagacgccga gcgcgcgcca gtcgaagctg 1140
acgcggggcg tgggcaaaaag gtgctggtac gaaacgtcgt ctaacggcat ggcgagccaa 1200
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<210> 20

<211> 392

<212> PRT

<213> Mycobacterium tuberculosis

<220>

<223> MTB40 (HTCC#1)

<400> 20

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  1           5           10          15
Leu Tyr Asp Leu Leu Gly Ile Gly Ile Pro Asn Gln Gly Gly Ile Leu
      20          25          30
Tyr Ser Ser Leu Glu Tyr Phe Glu Lys Ala Leu Glu Glu Leu Ala Ala
      35          40          45
Ala Phe Pro Gly Asp Gly Trp Leu Gly Ser Ala Ala Asp Lys Tyr Ala
      50          55          60
Gly Lys Asn Arg Asn His Val Asn Phe Phe Gln Glu Leu Ala Asp Leu
      65          70          75          80
Asp Arg Gln Leu Ile Ser Leu Ile His Asp Gln Ala Asn Ala Val Gln
      85          90          95
Thr Thr Arg Asp Ile Leu Glu Gly Ala Lys Lys Gly Leu Glu Phe Val
      100         105         110
Arg Pro Val Ala Val Asp Leu Thr Tyr Ile Pro Val Val Gly His Ala
      115         120         125
Leu Ser Ala Ala Phe Gln Ala Pro Phe Cys Ala Gly Ala Met Ala Val
      130         135         140
Val Gly Gly Ala Leu Ala Tyr Leu Val Val Lys Thr Leu Ile Asn Ala
      145         150         155         160
Thr Gln Leu Leu Lys Leu Leu Ala Lys Leu Ala Glu Leu Val Ala Ala
      165         170         175
Ala Ile Ala Asp Ile Ile Ser Asp Val Ala Asp Ile Ile Lys Gly Thr
      180         185         190
Leu Gly Glu Val Trp Glu Phe Ile Thr Asn Ala Leu Asn Gly Leu Lys
      195         200         205
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Glu	Leu	Trp	Asp	Lys	Leu	Thr	Gly	Trp	Val	Thr	Gly	Leu	Phe	Ser	Arg
210						215					220				
Gly	Trp	Ser	Asn	Leu	Glu	Ser	Phe	Phe	Ala	Gly	Val	Pro	Gly	Leu	Thr
225				230						235					240
Gly	Ala	Thr	Ser	Gly	Leu	Ser	Gln	Val	Thr	Gly	Leu	Phe	Gly	Ala	Ala
				245					250					255	
Gly	Leu	Ser	Ala	Ser	Ser	Gly	Leu	Ala	His	Ala	Asp	Ser	Leu	Ala	Ser
			260					265					270		
Ser	Ala	Ser	Leu	Pro	Ala	Leu	Ala	Gly	Ile	Gly	Gly	Gly	Ser	Gly	Phe
		275					280					285			
Gly	Gly	Leu	Pro	Ser	Leu	Ala	Gln	Val	His	Ala	Ala	Ser	Thr	Arg	Gln
290						295					300				
Ala	Leu	Arg	Pro	Arg	Ala	Asp	Gly	Pro	Val	Gly	Ala	Ala	Ala	Glu	Gln
305					310					315					320
Val	Gly	Gly	Gln	Ser	Gln	Leu	Val	Ser	Ala	Gln	Gly	Ser	Gln	Gly	Met
				325					330					335	
Gly	Gly	Pro	Val	Gly	Met	Gly	Gly	Met	His	Pro	Ser	Ser	Gly	Ala	Ser
			340					345					350		
Lys	Gly	Thr	Thr	Thr	Lys	Lys	Tyr	Ser	Glu	Gly	Ala	Ala	Ala	Gly	Thr
		355					360					365			
Glu	Asp	Ala	Glu	Arg	Ala	Pro	Val	Glu	Ala	Asp	Ala	Gly	Gly	Gly	Gln
370						375					380				
Lys	Val	Leu	Val	Arg	Asn	Val	Val								
385					390										

<210> 21
 <211> 1441
 <212> DNA
 <213> Mycobacterium tuberculosis

<220>
 <223> MTB41 (MTCC#2)

<400> 21
 gaggttgctg gcaatggatt tcgggctttt acctccggaa gtgaattcaa gccgaatgta 60
 ttccgggtccg gggccggagt cgatgctagc cgccgcggcc gcctggggacg gtgtggccgc 120
 ggagttgact tccgccgcgg tctcgtatgg atcgggtggtg tcgacgctga tcgttgagcc 180
 gtggatgggg ccggcggcgg ccgcgatggc ggccgcggca acgccgatg tgggggtggct 240
 ggccgccaag gcggcgctgg cgaaggagac ggccacacag gcgagggcag cggcggaagc 300
 gtttgggacg gcgttcgcga tgacggtgcc accatccctc gtcgcggcca accgcagccg 360
 gttgatgtcg ctggctgcgg cgaacattct ggggcaaaac agtgcggcga tcgcggctac 420
 ccaggccgag tatgccgaaa tgtgggcccc agacgctgcc gtgatgtaca gctatgaggg 480
 ggcactctcg gccgcgtcgg cgttgccgcc gttcactcca cccgtgcaag gcaccggccc 540
 ggccggggccc gcggccgcag ccgcggcgac ccaagccgcc ggtgcggggc cgttgcgga 600
 tgcacaggcg aactggccc agctgcccc ggggatcctg agcgacattc tgtccgcatt 660
 ggccgccaac gctgatccgc tgacatcggg actggtgggg atcgcgctga ccctcaacct 720
 gcaagtcgga tccgctcagc cgatagtgat cccaccccc atagggaat tggacgtgat 780
 cgcgctctac attgcatcca tcgcgaccgg cagcattgcg ctgcgatca cgaacacggc 840
 cagaccctgg cacatcgccc tatacgggaa cgccggcggg ctgggaccga cgcagggcca 900
 tccactgagt tcggcgaccg acgagccgga gccgcactgg ggccccttcg ggggcgcggc 960
 gccggtgtcc gcgggcgtcg gccacgcagc attagtcgga gcgttgctcg tgccgcacag 1020
 ctggaccacg gccgccccgg agatccagct cgccgttcag gcaacacca ccttcagctc 1080
 cagcgccggc gccgaccgga cggccctaaa cgggatgccg gcaggcctgc tcagcgggat 1140
 ggctttggcg agcctggccg cacgcggcac gacgggcggg ggcggcacc gttagcggac 1200
 cagcactgac ggccaagagg acggccgcaa acccccggta gttgtgatta gagagcagcc 1260
 gccgcccgga aacccccgcg ggtaaaagtc tccacaacct tcgtcgccgc gcggaaaatg 1320
 cctggtgagc gtggctatcc gacgggcgtg ccacaccgt tgtagtacg tacggctatg 1380
 gacgacggtg tctggattct cggcggctat cagagcgatt ttgctcgcaa cctcagcaaa 1440
 g 1441

<210> 22
 <211> 423
 <212> PRT
 <213> Mycobacterium tuberculosis

<220>
 <223> MTB41 (MTCC#2)

<400> 22
 Met Asp Phe Gly Leu Leu Pro Pro Glu Val Asn Ser Ser Arg Met Tyr
 1 5 10 15
 Ser Gly Pro Gly Pro Glu Ser Met Leu Ala Ala Ala Ala Trp Asp
 20 25 30
 Gly Val Ala Ala Glu Leu Thr Ser Ala Ala Val Ser Tyr Gly Ser Val
 35 40 45
 Val Ser Thr Leu Ile Val Glu Pro Trp Met Gly Pro Ala Ala Ala Ala
 50 55 60
 Met Ala Ala Ala Ala Thr Pro Tyr Val Gly Trp Leu Ala Ala Thr Ala
 65 70 75 80
 Ala Leu Ala Lys Glu Thr Ala Thr Gln Ala Arg Ala Ala Glu Ala
 85 90 95
 Phe Gly Thr Ala Phe Ala Met Thr Val Pro Pro Ser Leu Val Ala Ala
 100 105 110
 Asn Arg Ser Arg Leu Met Ser Leu Val Ala Ala Asn Ile Leu Gly Gln
 115 120 125
 Asn Ser Ala Ala Ile Ala Ala Thr Gln Ala Glu Tyr Ala Glu Met Trp
 130 135 140
 Ala Gln Asp Ala Ala Val Met Tyr Ser Tyr Glu Gly Ala Ser Ala Ala
 145 150 155 160
 Ala Ser Ala Leu Pro Pro Phe Thr Pro Pro Val Gln Gly Thr Gly Pro
 165 170 175
 Ala Gly Pro Ala Ala Ala Ala Ala Thr Gln Ala Ala Gly Ala Gly
 180 185 190
 Ala Val Ala Asp Ala Gln Ala Thr Leu Ala Gln Leu Pro Pro Gly Ile
 195 200 205
 Leu Ser Asp Ile Leu Ser Ala Leu Ala Ala Asn Ala Asp Pro Leu Thr
 210 215 220
 Ser Gly Leu Leu Gly Ile Ala Ser Thr Leu Asn Pro Gln Val Gly Ser
 225 230 235 240
 Ala Gln Pro Ile Val Ile Pro Thr Pro Ile Gly Glu Leu Asp Val Ile
 245 250 255
 Ala Leu Tyr Ile Ala Ser Ile Ala Thr Gly Ser Ile Ala Leu Ala Ile
 260 265 270
 Thr Asn Thr Ala Arg Pro Trp His Ile Gly Leu Tyr Gly Asn Ala Gly
 275 280 285
 Gly Leu Gly Pro Thr Gln Gly His Pro Leu Ser Ser Ala Thr Asp Glu
 290 295 300
 Pro Glu Pro His Trp Gly Pro Phe Gly Gly Ala Ala Pro Val Ser Ala
 305 310 315 320
 Gly Val Gly His Ala Ala Leu Val Gly Ala Leu Ser Val Pro His Ser
 325 330 335
 Trp Thr Thr Ala Ala Pro Glu Ile Gln Leu Ala Val Gln Ala Thr Pro
 340 345 350
 Thr Phe Ser Ser Ser Ala Gly Ala Asp Pro Thr Ala Leu Asn Gly Met
 355 360 365
 Pro Ala Gly Leu Leu Ser Gly Met Ala Leu Ala Ser Leu Ala Ala Arg
 370 375 380
 Gly Thr Thr Gly Gly Gly Gly Thr Arg Ser Gly Thr Ser Thr Asp Gly
 385 390 395 400
 Gln Glu Asp Gly Arg Lys Pro Pro Val Val Val Ile Arg Glu Gln Pro
 405 410 415

Pro Pro Gly Asn Pro Pro Arg
420

<210> 23
<211> 154
<212> DNA
<213> Mycobacterium tuberculosis

<220>
<223> ESAT-6

<400> 23
atgacagagc agcagtggaa tttcgcgggt atcgaggccg cggcaagcgc aatccagggga 60
aatgtcacgt ccattcattc cctccttgac gaggggaagc agtccctgac caagctcgca 120
gcggcctggg gcggtagcgg ttcggaagcg tacc 154

<210> 24
<211> 51
<212> PRT
<213> Mycobacterium tuberculosis

<220>
<223> ESAT-6

<400> 24
Met Thr Glu Gln Gln Trp Asn Phe Ala Gly Ile Glu Ala Ala Ala Ser
1 5 10 15
Ala Ile Gln Gly Asn Val Thr Ser Ile His Ser Leu Leu Asp Glu Gly
20 25 30
Lys Gln Ser Leu Thr Lys Leu Ala Ala Ala Trp Gly Gly Ser Gly Ser
35 40 45
Glu Ala Tyr
50

<210> 25
<211> 851
<212> DNA
<213> Mycobacterium tuberculosis

<220>
<223> MTB39 (TbH9) cDNA

<220>
<221> modified_base
<222> (767)
<223> n = g, a, c or t

<400> 25
ctgcagggtg gcgtggatga gcgtcaccgc ggggcaggcc gagctgaccg ccgcccaggt 60
ccgggttgct gcggcgccct acgagacggc gtatgggctg acggtgcccc cgccgggtgat 120
cgccgagaac cgtgctgaac tgatgattct gatagcgacc aacctcttg ggcaaaacac 180
cccggcgatc gcggtcaacg aggccgaata cggcgagatg tgggcccag acgccgcgcg 240
gatgtttggc tacgccgcgg cgacggcgac ggcgacggcg acgttgctgc cgttcgagga 300
ggcgccggag atgaccagcg cgggtgggct cctcgagcag gccgccgcgg tcgaggaggc 360
ctccgacacc gccgcggcga accagttgat gaacaatgtg cccagggcgc tgaaacagtt 420
ggcccagccc acgcagggca ccacgccttc ttccaagctg ggtggcctgt ggaagacggt 480
ctcgccgcat cggtcgccga tcagcaacat ggtgtcgatg gccacaacc acatgtcgat 540
gaccaactcg ggtgtgtcga tgaccaacac cttgagctcg atgttgaagg gctttgctcc 600

```

ggcgggcgcc gccagggccg tgcaaaccgc ggcgcaaaac ggggtccggg cgatgagctc 660
gctgggcagc tcgctgggtt cttcgggtct gggcggtggg gtggccgcca acttgggtcg 720
ggcggcctcg gtacggtatg gtcaccggga tggcggaata tatgcanagt ctggtcggcg 780
gaacggtggg ccggcgtaag gtttaccgcc gttttctgga tgcggtgaac ttcgtcaacg 840
gaaacagtta c 851

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<210> 26
<211> 263
<212> PRT
<213> Mycobacterium tuberculosis

```

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<220>
<223> MTB39 (TbH9)

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<220>
<221> MOD_RES
<222> (254)
<223> Xaa = any amino acid

```

```

<400> 26
Val Ala Trp Met Ser Val Thr Ala Gly Gln Ala Glu Leu Thr Ala Ala
1      5      10      15
Gln Val Arg Val Ala Ala Ala Tyr Glu Thr Ala Tyr Gly Leu Thr
20      25      30
Val Pro Pro Pro Val Ile Ala Glu Asn Arg Ala Glu Leu Met Ile Leu
35      40      45
Ile Ala Thr Asn Leu Leu Gly Gln Asn Thr Pro Ala Ile Ala Val Asn
50      55      60
Glu Ala Glu Tyr Gly Glu Met Trp Ala Gln Asp Ala Ala Ala Met Phe
65      70      75      80
Gly Tyr Ala Ala Ala Thr Ala Thr Ala Thr Ala Thr Leu Leu Pro Phe
85      90      95
Glu Glu Ala Pro Glu Met Thr Ser Ala Gly Gly Leu Leu Glu Gln Ala
100     105     110
Ala Ala Val Glu Glu Ala Ser Asp Thr Ala Ala Ala Asn Gln Leu Met
115     120     125
Asn Asn Val Pro Gln Ala Leu Lys Gln Leu Ala Gln Pro Thr Gln Gly
130     135     140
Thr Thr Pro Ser Ser Lys Leu Gly Gly Leu Trp Lys Thr Val Ser Pro
145     150     155     160
His Arg Ser Pro Ile Ser Asn Met Val Ser Met Ala Asn Asn His Met
165     170     175
Ser Met Thr Asn Ser Gly Val Ser Met Thr Asn Thr Leu Ser Ser Met
180     185     190
Leu Lys Gly Phe Ala Pro Ala Ala Ala Gln Ala Val Gln Thr Ala
195     200     205
Ala Gln Asn Gly Val Arg Ala Met Ser Ser Leu Gly Ser Ser Leu Gly
210     215     220
Ser Ser Gly Leu Gly Gly Gly Val Ala Ala Asn Leu Gly Arg Ala Ala
225     230     235     240
Ser Val Arg Tyr Gly His Arg Asp Gly Gly Lys Tyr Ala Xaa Ser Gly
245     250     255
Arg Arg Asn Gly Gly Pro Ala
260

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<210> 27
<211> 474
<212> DNA
<213> Mycobacterium tuberculosis

```

<220>
 <221> CDS
 <222> (16)..(450)
 <223> alpha-crystalline antigen

<400> 27
 attaggaggc atcaa atg gcc acc acc ctt ccc gtt cag cgc cac ccg cgg 51
 Met Ala Thr Thr Leu Pro Val Gln Arg His Pro Arg
 1 5 10

tcc ctc ttc ccc gag ttt tct gag ctg ttc gcg gcc ttc ccg tca ttc 99
 Ser Leu Phe Pro Glu Phe Ser Glu Leu Phe Ala Ala Phe Pro Ser Phe
 15 20 25

gcc gga ctc cgg ccc acc ttc gac acc cgg ttg atg cgg ctg gaa gac 147
 Ala Gly Leu Arg Pro Thr Phe Asp Thr Arg Leu Met Arg Leu Glu Asp
 30 35 40

gag atg aaa gag ggg cgc tac gag gta cgc gcg gag ctt ccc ggg gtc 195
 Glu Met Lys Glu Gly Arg Tyr Glu Val Arg Ala Glu Leu Pro Gly Val
 45 50 55 60

gac ccc gac aag gac gtc gac att atg gtc cgc gat ggt cag ctg acc 243
 Asp Pro Asp Lys Asp Val Asp Ile Met Val Arg Asp Gly Gln Leu Thr
 65 70 75

atc aag gcc gag cgc acc gag cag aag gac ttc gac ggt cgc tcg gaa 291
 Ile Lys Ala Glu Arg Thr Glu Gln Lys Asp Phe Asp Gly Arg Ser Glu
 80 85 90

ttc gcg tac ggt tcc ttc gtt cgc acg gtg tcg ctg ccg gta ggt gct 339
 Phe Ala Tyr Gly Ser Phe Val Arg Thr Val Ser Leu Pro Val Gly Ala
 95 100 105

gac gag gac gac att aag gcc acc tac gac aag ggc att ctt act gtg 387
 Asp Glu Asp Asp Ile Lys Ala Thr Tyr Asp Lys Gly Ile Leu Thr Val
 110 115 120

tcg gtg gcg gtt tcg gaa ggg aag cca acc gaa aag cac att cag atc 435
 Ser Val Ala Val Ser Glu Gly Lys Pro Thr Glu Lys His Ile Gln Ile
 125 130 135 140

cgg tcc acc aac tga ccactgggtc cgtgctgatg accg 474
 Arg Ser Thr Asn
 145

<210> 28
 <211> 144
 <212> PRT
 <213> Mycobacterium tuberculosis

<220>
 <223> alpha-crystalline antigen

<400> 28
 Met Ala Thr Thr Leu Pro Val Gln Arg His Pro Arg Ser Leu Phe Pro
 1 5 10 15
 Glu Phe Ser Glu Leu Phe Ala Ala Phe Pro Ser Phe Ala Gly Leu Arg
 20 25 30

Pro	Thr	Phe	Asp	Thr	Arg	Leu	Met	Arg	Leu	Glu	Asp	Glu	Met	Lys	Glu
		35					40					45			
Gly	Arg	Tyr	Glu	Val	Arg	Ala	Glu	Leu	Pro	Gly	Val	Asp	Pro	Asp	Lys
	50					55					60				
Asp	Val	Asp	Ile	Met	Val	Arg	Asp	Gly	Gln	Leu	Thr	Ile	Lys	Ala	Glu
	65				70					75					80
Arg	Thr	Glu	Gln	Lys	Asp	Phe	Asp	Gly	Arg	Ser	Glu	Phe	Ala	Tyr	Gly
				85				90						95	
Ser	Phe	Val	Arg	Thr	Val	Ser	Leu	Pro	Val	Gly	Ala	Asp	Glu	Asp	Asp
			100					105					110		
Ile	Lys	Ala	Thr	Tyr	Asp	Lys	Gly	Ile	Leu	Thr	Val	Ser	Val	Ala	Val
		115					120						125		
Ser	Glu	Gly	Lys	Pro	Thr	Glu	Lys	His	Ile	Gln	Ile	Arg	Ser	Thr	Asn
	130					135					140				

<210> 29

<211> 1211

<212> DNA

<213> Mycobacterium tuberculosis

<220>

<221> CDS

<222> (150)..(1172)

<223> 85 complex antigen (MTB85 complex antigen)

<400> 29

agggtgtcccg gccgacgctg aatcgtttagc caaccgcgat ctcgcgctgc ggccacgaca 60

ttcgaactga gcgtcctcgg tgtgtttcac tcgcccagaa cagattcgac cgcgtcgtgc 120

gcagatgaga	gttgggattg	gtagtagct	atg	acg	ttc	ttc	gaa	cag	gtg	cga						173
			Met	Thr	Phe	Phe	Glu	Gln	Val	Arg						
			1				5									

agg	ttg	cgg	agc	gca	gcg	aca	acc	ctg	ccg	cgc	cgc	gtg	gct	atc	gcg	221
Arg	Leu	Arg	Ser	Ala	Ala	Thr	Thr	Leu	Pro	Arg	Arg	Val	Ala	Ile	Ala	
	10					15					20					

gct	atg	ggg	gct	gtc	ctg	gtt	tac	ggg	ctg	gtc	ggg	acc	ttc	ggc	ggg	269
Ala	Met	Gly	Ala	Val	Leu	Val	Tyr	Gly	Leu	Val	Gly	Thr	Phe	Gly	Gly	
	25				30					35					40	

ccg	gcc	acc	gcg	ggc	gca	ttc	tct	agg	ccc	ggg	ctt	cca	gtg	gaa	tat	317
Pro	Ala	Thr	Ala	Gly	Ala	Phe	Ser	Arg	Pro	Gly	Leu	Pro	Val	Glu	Tyr	
			45						50					55		

ctg	cag	gtg	cca	tcc	gcg	tcg	atg	ggc	cgc	gac	atc	aag	gtc	cag	ttc	365
Leu	Gln	Val	Pro	Ser	Ala	Ser	Met	Gly	Arg	Asp	Ile	Lys	Val	Gln	Phe	
			60					65					70			

cag	ggc	ggc	gga	ccg	cac	gcg	gtc	tac	ctg	ctc	gac	ggg	ctg	cgg	gcc	413
Gln	Gly	Gly	Gly	Pro	His	Ala	Val	Tyr	Leu	Leu	Asp	Gly	Leu	Arg	Ala	
		75					80					85				

cag	gat	gac	tac	aac	ggc	tgg	gac	atc	aac	acc	ccg	gcc	ttc	gag	gag	461
Gln	Asp	Asp	Tyr	Asn	Gly	Trp	Asp	Ile	Asn	Thr	Pro	Ala	Phe	Glu	Glu	
	90					95					100					

tac tac cag tca ggg ttg tcg gtg atc atg ccc gtg ggc ggc caa tcc	509
Tyr Tyr Gln Ser Gly Leu Ser Val Ile Met Pro Val Gly Gly Gln Ser	
105 110 115 120	
agt ttc tac acc gac tgg tat cag ccc tcg cag agc aac ggc cag aac	557
Ser Phe Tyr Thr Asp Trp Tyr Gln Pro Ser Gln Ser Asn Gly Gln Asn	
125 130 135	
tac acc tac aag tgg gag acc ttc ctt acc aga gag atg ccc gcc tgg	605
Tyr Thr Tyr Lys Trp Glu Thr Phe Leu Thr Arg Glu Met Pro Ala Trp	
140 145 150	
cta cag gcc aac aag ggc gtg tcc ccg aca ggc aac gcg gcg gtg ggt	653
Leu Gln Ala Asn Lys Gly Val Ser Pro Thr Gly Asn Ala Ala Val Gly	
155 160 165	
ctt tcg atg tcg ggc ggt tcc gcg ctg atc ctg gcc gcg tac tac ccg	701
Leu Ser Met Ser Gly Gly Ser Ala Leu Ile Leu Ala Ala Tyr Tyr Pro	
170 175 180	
cag cag ttc ccg tac gcc gcg tcg ttg tcg ggc ttc ctc aac ccg tcc	749
Gln Gln Phe Pro Tyr Ala Ala Ser Leu Ser Gly Phe Leu Asn Pro Ser	
185 190 195 200	
gag ggc tgg tgg ccg acg ctg atc ggc ctg gcg atg aac gac tcg ggc	797
Glu Gly Trp Trp Pro Thr Leu Ile Gly Leu Ala Met Asn Asp Ser Gly	
205 210 215	
ggt tac aac gcc aac agc atg tgg ggt ccg tcc agc gac ccg gcc tgg	845
Gly Tyr Asn Ala Asn Ser Met Trp Gly Pro Ser Ser Asp Pro Ala Trp	
220 225 230	
aag cgc aac gac cca atg gtt cag att ccc cgc ctg gtc gcc aac aac	893
Lys Arg Asn Asp Pro Met Val Gln Ile Pro Arg Leu Val Ala Asn Asn	
235 240 245	
acc cgg atc tgg gtg tac tgc ggt aac ggc aca ccc agc gac ctc ggc	941
Thr Arg Ile Trp Val Tyr Cys Gly Asn Gly Thr Pro Ser Asp Leu Gly	
250 255 260	
ggc gac aac ata ccg gcg aag ttc ctg gaa ggc ctc acc ctg cgc acc	989
Gly Asp Asn Ile Pro Ala Lys Phe Leu Glu Gly Leu Thr Leu Arg Thr	
265 270 275 280	
aac cag acc ttc ccg gac acc tac gcg gcc gac ggt gga cgc aac ggg	1037
Asn Gln Thr Phe Arg Asp Thr Tyr Ala Ala Asp Gly Gly Arg Asn Gly	
285 290 295	
gtg ttt aac ttc ccg ccc aac gga aca cac tcg tgg ccc tac tgg aac	1085
Val Phe Asn Phe Pro Pro Asn Gly Thr His Ser Trp Pro Tyr Trp Asn	
300 305 310	
gag cag ctg gtc gcc atg aag gcc gat atc cag cat gtg ctc aac ggc	1133
Glu Gln Leu Val Ala Met Lys Ala Asp Ile Gln His Val Leu Asn Gly	
315 320 325	
gcg aca ccc ccg gcc gcc cct gct gcg ccg gcc gcc tga gccagcaagc	1182
Ala Thr Pro Pro Ala Ala Pro Ala Ala Pro Ala Ala	
330 335 340	
cagcatcggc agcagcgcaa cggccagcg	1211

<210> 30
 <211> 340
 <212> PRT
 <213> Mycobacterium tuberculosis

<220>
 <223> 85 complex antigen (MTB85 complex antigen)

<400> 30
 Met Thr Phe Phe Glu Gln Val Arg Arg Leu Arg Ser Ala Ala Thr Thr
 1 5 10 15
 Leu Pro Arg Arg Val Ala Ile Ala Ala Met Gly Ala Val Leu Val Tyr
 20 25 30
 Gly Leu Val Gly Thr Phe Gly Gly Pro Ala Thr Ala Gly Ala Phe Ser
 35 40 45
 Arg Pro Gly Leu Pro Val Glu Tyr Leu Gln Val Pro Ser Ala Ser Met
 50 55 60
 Gly Arg Asp Ile Lys Val Gln Phe Gln Gly Gly Gly Pro His Ala Val
 65 70 75 80
 Tyr Leu Leu Asp Gly Leu Arg Ala Gln Asp Asp Tyr Asn Gly Trp Asp
 85 90 95
 Ile Asn Thr Pro Ala Phe Glu Glu Tyr Tyr Gln Ser Gly Leu Ser Val
 100 105 110
 Ile Met Pro Val Gly Gly Gln Ser Ser Phe Tyr Thr Asp Trp Tyr Gln
 115 120 125
 Pro Ser Gln Ser Asn Gly Gln Asn Tyr Thr Tyr Lys Trp Glu Thr Phe
 130 135 140
 Leu Thr Arg Glu Met Pro Ala Trp Leu Gln Ala Asn Lys Gly Val Ser
 145 150 155 160
 Pro Thr Gly Asn Ala Ala Val Gly Leu Ser Met Ser Gly Gly Ser Ala
 165 170 175
 Leu Ile Leu Ala Ala Tyr Tyr Pro Gln Gln Phe Pro Tyr Ala Ala Ser
 180 185 190
 Leu Ser Gly Phe Leu Asn Pro Ser Glu Gly Trp Trp Pro Thr Leu Ile
 195 200 205
 Gly Leu Ala Met Asn Asp Ser Gly Gly Tyr Asn Ala Asn Ser Met Trp
 210 215 220
 Gly Pro Ser Ser Asp Pro Ala Trp Lys Arg Asn Asp Pro Met Val Gln
 225 230 235 240
 Ile Pro Arg Leu Val Ala Asn Asn Thr Arg Ile Trp Val Tyr Cys Gly
 245 250 255
 Asn Gly Thr Pro Ser Asp Leu Gly Gly Asp Asn Ile Pro Ala Lys Phe
 260 265 270
 Leu Glu Gly Leu Thr Leu Arg Thr Asn Gln Thr Phe Arg Asp Thr Tyr
 275 280 285
 Ala Ala Asp Gly Gly Arg Asn Gly Val Phe Asn Phe Pro Pro Asn Gly
 290 295 300
 Thr His Ser Trp Pro Tyr Trp Asn Glu Gln Leu Val Ala Met Lys Ala
 305 310 315 320
 Asp Ile Gln His Val Leu Asn Gly Ala Thr Pro Pro Ala Ala Pro Ala
 325 330 335
 Ala Pro Ala Ala
 340